In the Specification

Please replace the paragraph at page 8, line 16 through page 9, line 6 with the following paragraph:

The nucleic acid molecules of the invention can comprise, in addition to sequences identified by SEQ ID NO or sequences related to these by variations and by hybridization as described herein, other sequences encoding unrelated (heterologous -- that is, with insignificant sequence similarity to a Ferroportin1) polypeptides or peptides. These peptides or polypeptides can be whole proteins, as occur naturally or as have been modified by design. Together, the nucleic acid sequences make up genes for hybrid or fusion proteins. For example, an unrelated marker sequence that facilitates purification (e.g., by affinity column) of the fused polypeptide can be encoded. In certain embodiments of the invention, the marker sequence can be a hexa-histidine peptide, as provided in the pQE vector (Qiagen, Inc.) and described in Gentz *et al., Proc. Natl. Acad. Sci. USA 86*: 821-824 (1989), or an HA tag (Wilson *et al., Cell 37*: 767 (1984)), or a sequence encoding glutathione S-transferase of *Schistosoma japonicum* (vectors available from Pharmacia; see Smith, D.B. and Johnson K.S., *Gene 67*:31 (1988) and Kaelin, W.G. *et al., Cell 70*:351 (1992)). For additional applications, the unrelated nucleic acid sequence can encode a peptide or polypeptide which is immunogenic or which enhances the immunogenicity of the fusion protein or polypeptide. Nucleic acids of the invention also include, but are not limited to, nucleic acids comprising a structural gene and its naturally associated sequences that control gene expression.

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Please replace the paragraph at page 20, line 8 through page 21, line 17 with the following paragraph:

The comparison of sequences and determination of percent similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects,* Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis*

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of Sequence Data, Part 1, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology,* von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereaux, J., eds., M. Stockton Press, New York, 1991). In a preferred embodiment, the percent similarity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the Wisconsin Package Version 10.0, Genetics Computer Group (GCG), Madison WI, using, for example, a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent similarity between two nucleotide sequences is determined using the GAP program in the Wisconsin Package (Devereux, J., *et al.*, *Nucleic Acids Res. 12(1)*:387 (1984)), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent similarity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (*CABIOS, 4*:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Please replace the paragraph at page 21, line 18 through page 22, line 6 with the following paragraph:

The nucleic acids and protein sequences of the present invention can further be used as a "query sequence" to perform a search against databases to, for example, identify other family members or related sequences. Such searches can be performed using the BLASTN, BLASTP, BLASTX, TBLASTN, TBLASTX programs (version 2.0) or PSI-BLAST 2.1 programs based on Altschul, *et al.* (*J. Mol. Biol. 215*:403-10 (1990)). BLAST nucleotide searches can be performed with the BLASTN program, for example, with default parameters matrix = BIOSUM62, gap existence cost = 11, per residue gap cost = 1, lambda ratio = 0.85, filtered, to obtain nucleotide sequences homologous to (with calculatably significant similarity to) the nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, for example, with default parameters scoring matrix = BIOSUM62, word size = 3, E value = 10, gap

costs = 11,1 and alignments = 50, to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al., (Nucleic Acids Res. 25*(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

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Please replace the paragraph at page 30, line 26 through page 31, line 12 with the following paragraph:

Isolated Ferroportin1 protein or, an antigenically similar portion thereof, especially a portion that is soluble (e.g., a peptide or a fusion polypeptide comprising at least 10 contiguous amino acid residues of a Ferroportin1), can be used in a method to select and identify molecules which bind specifically to the Ferroportin1. Fusion proteins comprising all of, or a portion of, the Ferroportin1 linked to a second moiety not occurring in the Ferroportin1 as found in nature, can be prepared for use in another embodiment of the method. Suitable fusion proteins for this purpose include those in which the second moiety comprises an affinity ligand (e.g., an enzyme, antigen, epitope). Ferroportin1 fusion proteins can be produced by the insertion of a gene encoding the Ferroportin1 or a variant thereof, or a suitable portion of such gene into a suitable expression vector which encodes an affinity ligand (e.g., pGEX-4T-2 and pET-15b, encoding glutathione S-transferase and His-Tag affinity ligands, respectively). The expression vector can be introduced into a suitable host cell for expression. Host cells are lysed and the lysate, containing fusion protein, can be bound to a suitable affinity matrix by contacting the lysate with an affinity matrix.

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Please replace the paragraph at page 40, lines 6 through 20 with the following paragraph:

Another embodiment of the invention is a method for inhibiting iron export in Ferroportin1-expressing cells of a mammal (e.g., a human), comprising administering to the

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